PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

In re Application of:	)	
	)	
Lynn Adams *et al.*	)	Group Art Unit: 1647
	)	
Serial No. 09/512,260	)	Examiner: R. Deberry
	)	
Filed: February 24, 2000	)	Atty. Dkt. No. 003037.86702

For: **ENHANCERS OF CFTR CHLORIDE CHANNEL FUNCTION**

BRIEF ON APPEAL

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BRIEF ON APPEAL

Mail Stop Appeal Brief - Patents
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

An original and two copies of this brief are submitted along with the fee of $160.00. Appellants filed the Notice of Appeal on April 9, 2003. Thus a petition for a one-month extension of time also accompanies this brief. No other fee is believed to be due. If any other fee is required, please charge our Deposit Account No. 19-0733.

REAL PARTIES IN INTEREST

The real party in interest in this application is Case Western Reserve University, to which this invention is assigned.

RELATED APPEALS AND INTERFERENCES

There are no related appeals or interferences.

STATUS OF CLAIMS

Claims 8-34 are canceled. Claims 1-6 stand rejected and claim 7 is objected to as being dependent on a rejected claim. Claims 1-6 are the subject of this appeal and are listed in Appendix I.

STATUS OF AMENDMENTS

Claims 1 and 2 were amended and claims 8-34 were canceled in an Amendment After Final Rejection filed January 9, 2003. An Advisory Action mailed February 14, 2003 indicated that the amendments to claims 1 and 2 would not be entered.

SUMMARY OF THE INVENTION

Cystic fibrosis is a genetic disease commonly characterized by excessive production of thick mucus in the airways. The genetic defect that causes cystic fibrosis is a mutation in the gene encoding CFTR, a chloride channel located in the apical membrane of epithelial cells. (Page 1, lines 13-14.) Approximately 25% of the known mutations in CFTR produce a mutant protein that is transported to the apical membrane of epithelial cells but that has only low-level activity. (Page 2, line 24 to page 3, line 2.)

The invention is directed toward isolated polypeptides comprising a portion of cystic fibrosis transmembrane conductance regulator (CFTR) protein. (Page 3, lines 11-13.) The portion consists of between 18 and 100 amino acid residues. (Page 6, lines 18-23.) The portion

comprises 18 amino acid residues as shown in SEQ ID NO:1. (Page 3, lines 14-15.) The polypeptides of the invention are used to enhance the function of wild type or mutant CFTR proteins that are transported to the apical membrane but that have only low-level activity. (Page 7, lines 11-12.)

ISSUES

1. Tsui does not anticipate properly construed claims 1 and 2 because Tsui does not expressly or inherently teach a portion of CFTR protein that consists of between 18 and 100 amino acid residues.

2. The combination of Tsui, Welsh, and Langel does not render properly construed claims 3-6 obvious because it does not teach or suggest a portion of CFTR protein that consists of between 18 and 100 amino acid residues.

GROUPING OF CLAIMS

- Claims 1 and 2 stand or fall together with respect to issue 1.
- Claims 3-6 stand or fall together with respect to issue 2.

ARGUMENT

1. Tsui does not anticipate properly construed claims 1 and 2 because Tsui does not expressly or inherently teach a portion of CFTR protein that consists of between 18 and 100 amino acid residues.

Claims 1 and 2 stand rejected under 35 U.S.C. § 102(e) as anticipated by Tsui *et al.*, U.S. Patent 5,776,677 ("Tsui").

Before addressing the issue of whether claims are patentable they must be construed. *Finnigan Corporation v. United States International Trade Commission*, 180 F.3d 1354 (Fed. Cir. 1999). The M.P.E.P. and patent laws provide guidance to the Patent Office on proper construction of claims. During examination of a patent application the Patent Office construes

the pending claims giving them "the broadest reasonable interpretation consistent with the specification." M.P.E.P. § 2111. Each claim is an entity which must be considered as a whole. *General Foods v. Studiengesellschaft Kohle MbH*, 972 F.2d 1272 (Fed. Cir. 1992). All limitations in a claim must be considered meaningful. *Lantech, Inc. v. Keip Machine Company*, F.3d 542 (Fed. Cir. 1994) citing *Perkin-Elmer Corporation v. Westinghouse Electric Corporation*, F.2d 1528 (Fed. Cir. 1987). The words of the claim must be given their plain meaning unless applicant has provided a clear definition in the specification. *In re Zletz*, 893 F.2d 319 (Fed. Cir. 1989).

Claims 1 and 2 recite:

> 1. An isolated polypeptide comprising a portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein wherein said portion consists of between 18 and 100 amino acid residues, wherein said portion comprises 18 amino acid residues as shown in SEQ ID NO: 1.
>
> 2. The polypeptide of claim 1 wherein the portion of CFTR protein comprises 22 amino acid residues as shown in SEQ ID NO: 2.

Claims 1 and 2 are directed to isolated polypeptides. Claim 1 recites an isolated polypeptide that comprises a "portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein." (Claim 1, lines 1-2.) The recited portion is within an isolated polypeptide because the claim recites that the "isolated polypeptide compris[es] a portion of the CFTR protein". This indicates that the polypeptide may also contain other sequences. A "portion" is a part separated from a whole. See Webster's II New College Dictionary, Copyright 2001 by Houghton Mifflin Company, definition 2; Exhibit A. Thus the plain meaning of a "portion" of CFTR protein is a part separated from a whole CFTR protein. Claims 1 and 2 recite two characteristics of the "portion" of CFTR protein: (1) the portion of CFTR protein "consists of

between 18 and 100 amino acid residues" (claim 1, lines 2-3); and (2) the portion of CFTR protein "comprises 18 amino acid residues as shown in SEQ ID NO:1" (claim 1, line 3) or "comprises 22 amino acid residues as shown in SEQ ID NO:2" (claim 2, lines 1-2). "Consists of" is closed claim language which limits the "portion," excluding any number of amino acid residues more than 100 in the portion. Thus, claims 1 and 2 require that the portion of CFTR protein contain no more than 100 amino acid residues and that it comprise the 18 amino acid residues as shown in SEQ ID NO:1 (claim 1) or the 22 amino acid residues as shown in SEQ ID NO:22 (claim 2). As mentioned above, the isolated polypeptide that comprises the portion of CFTR may contain other sequences, however, due to the constraints on the term "portion," the other sequences must be non-CFTR sequences. The "portion" of CFTR in the polypeptide may not contain more of CFTR than 100 amino acids, because that would deprive the term "said portion consists of between 18 and 100 amino acids" of any meaning. Moreover, the isolated polypeptide can certainly not comprise full-length CFTR because that would not give meaning to the recited term "a portion of CFTR."[1] Thus properly construed claims 1 and 2 are directed to an isolated polypeptide that comprises no more than 100 amino acids of CFTR protein and may optionally contain other non-CFTR sequences.

Anticipation under 35 U.S.C. § 102 requires that "each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." *Verdegaal Bros., Inc. v. Union Oil Co.*, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987).

Tsui teaches the nucleic acid and amino acid sequence of full-length CFTR polypeptide:

[1] The Patent Office apparently agrees with the construction of the terms "[a]n isolated polypeptide comprising a portion of CFTR protein" as not reading on full-length CFTR because it has found claim 7 to be allowable over full-length CFTR, and claim 7 contains the same terms.

"an ORF [open reading frame] capable of encoding a polypeptide of 1480 amino acids (FIG. 1)." (Column 21, lines 24-27.) Tsui also teaches portions of the CFTR protein. The portions of the CFTR protein are disclosed as SEQ ID NOs:18-43. Each of these portions is 109, 110, or 111 amino acid residues in length. See § (i)(A) for each of SEQ ID NO:s:18-43 of Tsui.

By definition, Tsui's full-length CFTR is not a portion. Moreover, the full-length, 1480 amino acid-residue CFTR sequence taught by Tsui is far larger than the 100 amino acid residue maximum of the portion of CFTR protein recited in claim 1 and dependent claim 2 ("wherein said portion consists of between 18 and 100 amino acid residues"). Thus the full-length CFTR polypeptide taught by Tsui is not a polypeptide comprising a "portion" of CFTR that "consists of between 18 and 100 amino acid residues."

Tsui's polypeptides of 109, 110, or 111 amino acid residues of CFTR protein are also larger than the at-most 100 amino acid residues of the portion of CFTR protein recited in claim 1 and dependent claim 2. Thus, Tsui does not teach any polypeptide that comprises a "portion" of CFTR that "consists of between 18 and 100 amino acid residues" as recited in claims 1 and 2.

Furthermore, the CFTR polypeptides taught by Tsui as SEQ ID NOs:18-43 do not comprise "18 amino acid residues as shown in SEQ ID NO:1" as required by claim 1. The amino acid sequence of each of Tsui's SEQ ID NOs:18-43 was aligned with SEQ ID NO:1 of the instant application using the Basic Local Alignment Search Tool algorithm (Altschul *et al.* (1990) *J. Mol. Biol. 215*(3):403-10). None of Tsui's SEQ ID NOs:18-43 share amino acid sequence identity with the 18 amino acid residues of SEQ ID NO:1. See Exhibit B. The 18 amino acid residues of SEQ ID NO:1 are included in the 22 amino acid residues of SEQ ID NO:2. Because none of Tsui's SEQ ID NOs:18-43 comprise the 18 amino acid residues of SEQ ID NO:1, none of Tsui's SEQ ID NOs:18-43 comprise the 22 amino acid residues of SEQ ID

NO:2. Thus none of Tsui's SEQ ID NOs:18-43 are polypeptides that comprise a portion of CFTR protein that "comprises 18 amino acid residues as shown in SEQ ID NO:1" (as required by claim 1) or "comprises 22 amino acid residues as shown in SEQ ID NO:2" (as required by claim 2).

In asserting that Tsui anticipates claims 1 and 2, the Patent Office has ignored the well-established rules of proper claim construction and assigned no meaning to the recitation that the polypeptide comprises a "portion" of CFTR protein that "consists of between 18 and 100 amino acid residues." Tsui does not explicitly or inherently disclose each and every element of properly construed claims 1 and 2. The rejection should be reversed.

2. The combination of Tsui, Welsh, and Langel does not render properly construed claims 3-6 obvious because it does not teach or suggest a portion of CFTR protein that consists of between 18 and 100 amino acid residues.

Obviousness is a question of law based on findings of fact. *Graham v. John Deere Company*, 383 U.S. 1, 17-18 (1966). An obviousness analysis requires determination of certain facts:

> Under § 103, the scope and content of the prior art are to be determined; differences between the prior art and the claims at issue are to be ascertained; and the level of ordinary skill in the pertinent art resolved.

Id. In rejecting claims under 35 U.S.C. § 103, the examiner bears the initial burden of presenting a *prima facie* case of obviousness. *In re Oetiker*, 977 F.2d 1443, 1445 (Fed. Cir. 1992). To establish *prima facie* obviousness of a claimed invention, all of the claim limitations must be taught or suggested by the prior art. *In re Royka*, 490 F.2d 981 (CCPA 1974).

The U.S. Patent and Trademark Office asserts that the combination of Tsui, in view of Welsh *et al.*, U.S. Patent WO 95/25796 ("Welsh"), and Langel *et al.*, 6,025,140 ("Langel")

renders claims 3-6 obvious under 35 U.S.C. § 103(a). The rejection over the combination of Tsui, Welsh, and Langel fails to meet the legal standard for obviousness because the combination does not teach or suggest a polypeptide comprising a portion of CFTR protein that "consists of between 18 and 100 amino acid residues."

Each of the rejected claims is directed to isolated polypeptides. Independent claim 1, discussed above, from which claims 3-6 depend, requires that an isolated polypeptide comprises a portion of CFTR protein. The portion has two recited characteristics. The portion consists of between 18 and 100 amino acid residues and the portion comprises the 18 amino acid residues as shown in SEQ ID NO:1. As discussed above, Tsui does not teach a polypeptide comprising a portion of CFTR protein that "consists of between 18 and 100 amino acid residues." Neither of the secondary references remedies this defect in Tsui.

Welsh teaches truncated CFTR proteins that retain CFTR protein activity. Welsh defines a truncated CFTR protein as a "polypeptide that exhibits CFTR activity [and] includes the MSD-1 [membrane spanning domain-1], NBD-1 [nucleotide binding domain-1] and R [regulator] domains of CFTR." (Page 18, lines 21-23.) This truncated CFTR protein does not consist of "between 18 and 100 amino acid residues" as required by claim 1. In fact, each of the MSD-1, NBD-1, and R domains of CFTR individually contains more than 100 amino acid residues. The MSD-1 domain contains 285 amino acid residues. "'MSD-1 or Membrane Spanning Domain-1' refers to the amino terminal membrane spanning domain of CFTR that includes an amino acid sequence that spans from about amino acid residue 76 to residue 360 of CFTR." (Page 19, line 23 to page 20, line 2.) The NBD-1 domain of CFTR protein contains 349 amino acid residues. "'NBD-1 or Nucleotide Binding Domain-1' refers to the amino terminal nucleotide binding domain of CFTR, including an amino acid sequence that spans from about amino acid residue

360 to residue 708 of full length CFTR." (Page 19, lines 15-18.) The R domain of CFTR protein contains 241 amino acid residues. "The R domain of CFTR, which, thus, regulates anion passage through the Cl^- channel, is encoded by exon 13 of the genomic CFTR gene, and includes a 241 amino acid sequence spanning from about amino acid residue 590 to residue 830 of full length CFTR." (Page 19, lines 7-11.) Thus Welsh's truncated CFTR proteins are not polypeptides that comprise a portion of CFTR that consist of "between 18 and 100 amino acid residues."

Langel also does not teach or suggest a polypeptide comprising a portion of CFTR protein as recited in claim 1. Langel teaches peptides that transport nucleic acid analogs across a lipid membrane and deliver the nucleic acid analogues to structures such as RNA, DNA, enzymes, receptors, or regulatory elements. (Column 5, lines 47-53.) Langel does not teach a CFTR protein or any portion of a CFTR protein and cannot remedy the defect of Tsui and Welsh.

Thus, Tsui, Welsh, and Langel neither alone nor in combination teach or suggest a polypeptide that comprises a portion of CFTR protein that "consists of between 18 and 100 amino acid residues" as recited in claim 1.

The Patent Office has ignored the recitation that the "portion" of the CFTR protein "consists of between 18 and 100 amino acid residues." As a result of doing so, the Patent Office has cited a combination of prior art that fails to teach or suggest all the limitations of the claims. Thus, a *prima facie* case of obviousness of claims 3-6 has not been made. The rejection should be reversed.

CONCLUSION

For the reasons given above, the rejection of claims 1 and 2 under 35 U.S.C. § 102(e) and

the rejection of claims 3-6 under 35 U.S.C. § 103(a) are improper. The Board of Patent Appeals and Interferences should reverse the rejections.

Respectfully submitted,

Date: July 9, 2003

By: _____
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Registration No. 47,660

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APPENDIX I. APPEALED CLAIMS

1. An isolated polypeptide comprising a portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein wherein said portion consists of between 18 and 100 amino acid residues, wherein said portion comprises 18 amino acid residues as shown in SEQ ID NO: 1.

2. The polypeptide of claim 1 wherein the portion of CFTR protein comprises 22 amino acid residues as shown in SEQ ID NO: 2.

3. The polypeptide of claim 1 wherein the polypeptide is fused to a membrane-penetrating peptide.

4. The polypeptide of claim 2 wherein the polypeptide is fused to a membrane-penetrating peptide.

5. The polypeptide of claim 3 wherein the membrane-penetrating peptide is selected from the group consisting of: VP-22 (SEQ ID NO: 3), (SEQ ID NO: 4), and (SEQ ID NO: 5).

6. The polypeptide of claim 4 wherein the membrane-penetrating peptide is selected from the group consisting of: VP-22 (SEQ ID NO: 3), (SEQ ID NO: 4), and (SEQ ID NO: 5).

7. The polypeptide of claim 1, wherein the portion of CFTR protein consists of a sequence of amino acid residues as shown in SEQ ID NO: 2, and wherein the portion is free of phosphorylation.

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Filed: February 24, 2000	)	Atty. Dkt. No. 003037.86702

For: **ENHANCERS OF CFTR CHLORIDE CHANNEL FUNCTION**

REQUEST FOR ADMITTANCE OF EXHIBITS UNDER 37 C.F.R. § 1.195

Assistant Director for Patents
Washington, D.C. 20231

Sir:

An appeal brief and the requisite fees are being filed concurrently with this paper. We believe no fee is due in connection with this request. If any fee is due, please charge our Deposit Account No. 19-0733.

Please admit exhibits A and B during consideration of the appealed claims.

Remarks

Please admit and consider exhibits A and B during consideration of the appealed claims.

Exhibit A. Exhibit A is a page from the Webster's II New College Dictionary containing the definition of "portion." It is provided to rebut the allegation of the Patent Office that the claims read on full-length cystic fibrosis transmembrane conductance regulator (CFTR) protein. Advisory Action, page 2, lines 10-11. Exhibit A was not submitted earlier because appellants

believed that the arguments and claim amendments submitted in response to the Office Action dated May 7, 2003 and in response to the Final Office Action dated October 9, 2002 were sufficient to clarify that the claims do not read on full-length CFTR and to overcome the rejections.

Exhibit B. Exhibit B presents the results of aligning SEQ ID NOs:18-43 taught by Tsui with SEQ ID NO:1 of the instant application using the Basic Local Alignment Search Tool algorithm. Claim 1, the only independent claim of the application requires that an isolated polypeptide comprise a portion of CFTR protein that "comprises 18 amino acid residues as shown in SEQ ID NO:1." The Exhibit provides evidence that none of the fragments of CFTR protein taught by Tsui contain SEQ ID NO:1 of the instant application. Exhibit B was not submitted earlier because appellants believed that the argument submitted in the response to Final Office Action would be sufficient to overcome the rejection of the claims over Tsui.

Entry of Exhibits A and B is respectfully requested.

Respectfully submitted,

Date: July 9, 2003

By: _____
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Webster's II

New College Dictionary

Houghton Mifflin Company
Boston • New York

ISBN 0-395-96214-5
ISBN 0-618-16903-2 (paper-over-boards binding)

Library of Congress Cataloging-in-Publication Data

Webster's II new college dictionary.
p. cm.
ISBN 0-395-70869-9 (alk. paper)
1. English language – Dictionaries. I. Webster's II new Riverside University dictionary
PE1628.W55164 1995
423–dc20 95-5833
CIP

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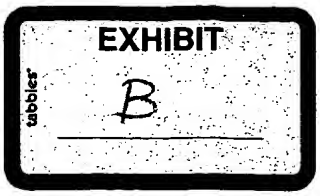
Printed in the United States

por·ter² (pôr′tər, pōr′-) *n.* [ME < OFr. *portier* < LLat. *portarius* < Lat. *porta*, gate.] *Chiefly Brit.* A gatekeeper : doorman.
por·ter³ (pôr′tər, pōr′-) *n.* [Short for *porter's beer.*] A dark beer resembling light stout, made from browned or charred malt.
por·ter·age (pôr′tər-ĭj, pōr′-) *n.* **1.** The carrying of parcels or goods as done by porters. **2.** The charge for such service.
por·ter·ess (pôr′tər-ĭs, pōr′-) *n. var. of* PORTRESS.
por·ter·house (pôr′tər-hous′, pōr′-) *n.* **1.** A 19th-cent. American alehouse or chophouse. **2.** A cut of beef from the thick end of the short loin, having a T-bone and a sizable piece of tenderloin.
porterhouse steak *n.* PORTERHOUSE 2.
port·fo·li·o (pôrt-fō′lē-ō′, pōrt-) *n., pl.* **-os.** [Ital. *portafoglio* : *portare*, to carry (< Lat.) + *foglio*, sheet < Lat. *folium*, leaf.] **1. a.** A portable case for holding papers, drawings, or photographs. **b.** The materials included in such a case, esp. when representative of one's work <a designer's *portfolio*> **2.** The office or post of a cabinet member or minister of state. **3.** A list of investments, securities, and commercial paper owned, as by a bank or individual investor.
port·hole (pôrt′hōl′, pōrt′-) *n.* **1.** A small, usu. circular window in a ship's side. **2.** An embrasure.
por·ti·co (pôr′tĭ-kō′, pōr′-) *n., pl.* **-coes** *or* **-cos.** [Ital. < Lat. *porticus* < *porta*, gate.] A walkway or porch with a roof supported by columns, often at the entrance of a building. **—por′ti·coed′** *adj.*
por·tière *or* **por·tiere** (pôr-tyâr′, pōr-) *n.* [Fr. < OFr., fem. of *portier*, porter < LLat. *portarius* < Lat. *porta*, gate.] A heavy curtain hung across a doorway.
por·tion (pôr′shən, pōr′-) *n.* [ME < OFr. < Lat. *portio.*] **1.** A part of a whole. **2.** A part separated from a whole. **3.** A part allotted to a person or group, as: **a.** A helping of food. **b.** The part of an estate received by an heir. **c.** A woman's dowry. **4.** One's destiny or fate. *—vt.* **-tioned, -tion·ing, -tions. 1.** To divide into parts or shares for distribution. **2.** To provide with a share, inheritance, or dowry. **—por′tion·a·ble** *adj.* **—por′tion·er** *n.* **—por′tion·less** *adj.*
Port·land cement (pôrt′lənd, pōrt′-) *n.* [After *Portland*, England, from its resemblance to limestone quarried there.] A hydraulic cement made by heating a mixture of limestone and clay, containing oxides of calcium, aluminum, iron, and silicon, in a kiln and pulverizing the resultant clinker.
port·ly (pôrt′lē, pōrt′-) *adj.* **-li·er, -li·est.** [< PORT⁵.] **1.** Corpulent : stout. **2.** *Archaic.* Stately : imposing. **—port′li·ness** *n.*
port·man·teau (pôrt-măn′tō, pōrt-, pōrt′măn-tō′, pōrt′-) *n., pl.* **-teaus** *or* **-teaux** (-tōz) [Fr. *portemanteau* < OFr. : *porter*, to carry (< Lat. *portare*) + *manteau*, cloak < Lat. *mantellum.*] *Chiefly Brit.* A large leather suitcase that opens into two hinged compartments.
portmanteau word *n.* A word formed by merging the sounds and meanings of two different words; e.g., *chortle*, from *chuckle* and *snort.*
port of call *n.* A port where ships dock in the course of voyages to load or unload cargo, obtain supplies, or undergo repairs.
port of entry *n.* A place where travelers or goods may enter or leave a country under official supervision.
por·trait (pôr′trĭt, -trāt′, pōr′-) *n.* [Fr. < OFr. < *portraire*, to portray.] **1.** A likeness of a person, as a painting or photograph, esp. one showing the face. **2.** A verbal picture or description, esp. of a person. *—adj. Computer Sci.* Of or relating to the orientation of a printed page that is taller than it is wide.
por·trait·ist (pôr′trə-tĭst, pōr-) *n.* One who makes portraits, esp. a painter or photographer.
por·trai·ture (pôr′trĭ-chŏŏr′, pōr′-) *n.* **1.** The art or practice of making portraits. **2.** A portrait. **3.** A group of portraits.
por·tray (pôr-trā′, pōr-) *vt.* **-trayed, -tray·ing, -trays.** [ME *portraien* < OFr. *portraire* < Lat. *protrahere*, to reveal : *pro-*, forth + *trahere*, to draw.] **1.** To make a picture of. **2.** To depict or describe in words. **3.** To represent dramatically, as on the stage. **—por·tray′a·ble** *adj.* **—por·tray′al** (-trā′əl, pōr-) *n.* **—por·tray′er** *n.*
por·tress (pôr′trĭs, pōr′-) *also* **por·ter·ess** (pôr′tər-ĭs, pōr′-) *n.* **1.** A woman porter or doorkeeper, esp. in a convent. **2.** A charwoman.
Port Sa·lut (pôr′ sä-lōō) *also* **Port du Sa·lut** (pôr′ dü sä-lōō′) *n.* [After *Port du Salut*, Trappist abbey in France.] A semihard fermented cheese made orig. by Trappist monks in France.
Por·tu·guese (pôr′chə-gēz′, -gēs′, pōr′-) *adj.* Of or relating to Portugal, its people, or their language. *—n., pl.* **Portuguese. 1. a.** A native or resident of Portugal. **b.** One of Portuguese descent. **2.** The Romance language of Portugal and Brazil.
Portuguese man-of-war *n.* A complex colonial organism of the genus *Physalia* of warm seas, with a bluish bladderlike float from which are suspended numerous long stinging tentacles capable of inflicting severe injury.
por·tu·lac·a (pôr′chə-lăk′ə, pōr′-) *n.* [NLat. *Portulaca*, genus name < Lat. *portulaca*, purslane < *portula*, dim. of *porta*, gate.] A plant of the genus *Portulaca*, bearing fleshy stems and leaves, esp. *P. grandiflora*, cultivated for its variously colored flowers that open only in sunlight.
pose¹ (pōz) *v.* **posed, pos·ing, pos·es.** [ME *posen* < OFr. *poser* < LLat. *pausare*, to rest < Lat. *pausa*, pause. —see PAUSE.] *—vi.* **1.** To assume or hold a position or posture, as in sitting for a portrait. **2.** To affect a particular mental attitude. **3.** To pretend to be other than what one is. *—vt.* **1.** To place (e.g., a model) in a specific position. **2.** To advance or put forward <*pose* a problem> *—n.* **1.** A bodily posture or position, esp. one assumed for an artist or photographer. **2.** An affected physical or mental attitude.
pose² (pōz) *vt.* **posed, pos·ing, pos·es.** [ME *apposen*, alteration of *opposen* < OFr. *opposer*, to oppose. —see OPPOSE.] To puzzle or confuse with a difficult question or problem.
Po·sei·don (pō-sīd′n) *n.* [Lat. < Gk. *Poseidōn.*] *Gk. Myth.* The god of the waters, earthquakes, and horses.
pos·er¹ (pō′zər) *n.* One who poses.
pos·er² (pō′zər) *n.* A baffling question or problem.
po·seur (pō-zœr′) *n.* [Fr. < OFr. *poser*, to pose. —see POSE¹.] One who assumes an attitude, character, or manner to impress others.
posh (pŏsh) *adj.* [Orig. unknown.] Fashionable and expensive.
pos·i·grade (pŏz′ĭ-grād′) *adj.* [POSI(TIVE) + (RETRO)GRADE.] Of, pertaining to, or being an auxiliary rocket on a spacecraft that provides additional thrust in the direction of the spacecraft's motion.
pos·it (pŏz′ĭt) *vt.* **-it·ed, -it·ing, -its.** [< Lat. *positus*, p.part. of *ponere*, to place.] **1.** To place in position. **2.** To present as a fact or assumption : POSTULATE.
po·si·tion (pə-zĭsh′ən) *n.* [OFr. < Lat. *positio* < *ponere*, to place.] **1.** A place or location. **2.** The right or appropriate place <The contestants were in *position.*> **3. a.** The way in which one is placed <in an inconspicuous *position*> **b.** The arrangement of bodily parts : POSTURE <a prone *position*> **4.** An advantageous place or location <race cars jockeying for *position*> **5.** A situation as it relates to the surrounding circumstances <not in a *position* to quibble> **6.** An attitude or point of view on a certain question. **7.** Social status. **8.** A post of employment : JOB. **9.** The area for which a particular player is responsible in a sport. **10. a.** The act or process of positing. **b.** The principle or proposition posited. *—vt.* **-tioned, -tion·ing, -tions.** To place in proper position. **—po·si′tion·al** *adj.* **—po·si′tion·er** *n.*
position paper *n.* **1.** A detailed policy report that usu. explains, justifies, or recommends a course of action. **2.** An aide-mémoire.
pos·i·tive (pŏz′ĭ-tĭv) *adj.* [ME < OFr. *positif* < Lat. *positivus*, formally laid down < *ponere*, to place.] **1.** Marked by or exhibiting certainty, acceptance, or affirmation <a *positive* reply> **2.** Measured or moving in a direction of increase, progress, or forward motion. **3.** Openly or explicitly laid down or expressed <a *positive* claim>. **4.** Admitting of no doubt : IRREFUTABLE. **5. a.** Determined or settled in opinion or assertion : CONFIDENT <a *positive* attitude> **b.** Overconfident : dogmatic. **6.** Formally or arbitrarily determined : PRESCRIBED. **7.** Concerned with practical rather than theoretical matters. **8.** Composed of or marked by the presence of distinctive qualities or attributes : REAL. **9.** *Philos.* Of or relating to positivism. **10.** *Informal.* Complete : utter <a *positive* angel> **11.** *Math.* Relating to or designating: **a.** A quantity greater than zero. **b.** The sign (+). **c.** A quantity, number, angle, or direction opposite to another designated as negative. **12.** *Physics.* Relating to or designating electric charge of a sign opposite to that of an electron. **13.** *Med.* Indicating the presence of a particular disease, condition, or organism <a *positive* TB test> **14.** *Biol.* Indicating or marked by response or motion toward the source of a stimulus. **15.** Having the areas of light and dark in their original and normal relationship, as in a photographic print made from a negative. **16.** Of, relating to, or denoting the simple uncompared degree of an adjective or adverb. **17.** Driven by or generating power directly through intermediate machine parts having little or no play. *—n.* **1.** Something positive. **2.** *Philos.* Something perceptible to the senses. **3.** *Math.* A quantity greater than zero. **4.** *Physics.* A positive electric charge. **5.** A photographic image in which the lights and darks appear as they do naturally. **6. a.** The uncompared degree of an adjective or adverb. **b.** A word in this degree. **—pos′i·tive·ly** *adv.* **—pos′i·tive·ness** *n.*
positive prescription *n. Law.* PRESCRIPTION 4a.
pos·i·tiv·ism (pŏz′ĭ-tĭ-vĭz′əm) *n.* **1. a.** A philosophical doctrine contending that sense perceptions are the only admissible basis of human knowledge and precise thought. **b.** The application of this doctrine in logic, epistemology, and ethics. **2.** The system of Auguste Comte designed to supersede theology and metaphysics and depending on a hierarchy of the sciences, beginning with mathematics and culminating in sociology. **3.** The quality or state of being positive. **—pos′i·tiv·ist** *n.* **—pos′i·tiv·is′tic** *adj.*
pos·i·tron (pŏz′ĭ-trŏn′) *n.* [POSI(TIVE) + (ELEC)TRON.] The antiparticle of the electron.
pos·i·tro·ni·um (pŏz′ĭ-trō′nē-əm) *n.* [NLat. < POSITRON.] A short-lived association of an electron and a positron bound together in a configuration resembling the hydrogen atom.
pos·se (pŏs′ē) *n.* [Short for Med. Lat. *posse comitatus*, power of the county.] **1.** A group of persons deputized by a sheriff to aid in law enforcement. **2.** A search party.
pos·sess (pə-zĕs′) *vt.* **-sessed, -sess·ing, -sess·es.** [ME *possessen* < OFr. *possesser* < Lat. *possidere* : *potis*, capable + *sedere*, to sit.] **1.** To have as property : OWN. **2.** To have as a quality, characteristic, or attribute <*possessed* much courage> **3.** To acquire mastery of or have knowledge of <*possess* secret information> **4.** To gain or exert influence over : DOMINATE <Rage *possessed* me.> **5.** To control or maintain in a given condition <*possessed* my equanimity despite the



Sequence 1=Tsui SEQ ID NO:18
F S L L G T P V L K D I N F K I E R G Q L L A V A G S T G A G K T S L L M M I M G I S F
C S Q F S W I M P G T I K E N I I F G V S Y D G E G G I T L S G G Q R A R I S L A R A V
Y K D A D L Y L L D S P F G Y L D V L T E K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

NCBI **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:19
YTEGGNAILENISFSISPGQRVGLLGRTGSGKSTLLSAFLRDSIT
LQQWRKAFGVIPQKVFIFSGTFRVDGGCVLSHGHKQLMCLAR
SVLSKAKILLLDEPSAHLDPVTYQ

Sequence 2=application SEQ ID NO:1
GLEISEEINEEDLKECFF

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:20
P S R K E V K I L K G L N L K V Q S G Q T V A L V G N S G C G K S T T V Q L M Q R I G
V V S Q E P V L F A T T I A E N I R Y G R E N V G E R G A Q L S G G Q K Q R I A I A R
A L V R N P K I L L L D E A T S A L D T E S E A

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:21
P T R P D I P V L Q G L S L E V K K G Q T L A L V G S S G C G K S T V V Q L L E R L G I
V S Q E P I L F D C S I A E N I A Y G D N S R G D K G T L L S G G Q K Q R I A I A R A L
V R Q P H I L L L D E A T S A L D T E S E K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:22
P S R S E V Q I L K G L N L K V K S G Q T V A L V G N S G C G K S T T V Q L M Q R I G
V V S Q E P V L F A T T I A E N I R Tyr G R E D V G E R G A Q L S G G Q K Q R I A I A R
A L V R N P K I L L L D E A T S A L D T E S E A

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 112

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:23
P T R P N I P V L Q G L S L E V K K G Q T L A L V G S S G C G K S T V V Q L L E R L G
E V S Q E P I L F D C S I A E N I A Y G D N S R G D K G T Q L S G G Q K Q R I A I A R A
L V R Q P H I L L L D E A T S A L D T E S E K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

NCBI **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:24
P S R A N I K I L K G L N L K V K S G Q T V A L V G N S G C G K S T T V Q L L Q R I G
V V S Q E P V L S F T T I A E N I R Y G R G V G D R G A Q L S G G Q K Q R I A I A R A
L V R N P K I L L L D E A T S A L D T E S E A

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 109

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:25
P T R A N V P N L Q G L S L E V K K G Q T L A L V G S S G C G K S T V V Q L L E R L G
I V S Q E P I L F D C S I A E N I A Y G D N S R G D K G T Q L S G G Q K Q R I A I A R A
L I R Q P R V L L L D E A T S A L D T E S E K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:26
D T R S D V E I Y K D L S F T L L K E G K T Y A F V G E S G C G K S T I L K L I E I G V
V S Q D P L L F S N S I K N N I K Y S L Y S L S N A S K L S G G Q K Q R I S I A R A I M
R N P K I L I L D E A T S S L D N K S E Y

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 109

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:27
I S R P N V P I Y K N L S F T C D S K K T T A I V G E T G S G K S T F M N L L L R F S I
V S Q E P M L F N M S I Y E N I K F G R E D A P Y G K S L S G G Q K Q R I A I A R A L
L R E P K I L L L D E A T S S L D S N S E K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 109

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:28
P S R P S E A V L K N V S L N F S A G Q F T F I V G K S G S G K S T L S N L L L R I T V
V E Q R C T L F N D T L R K N I L L G S T D S G T G G V T L S G G Q Q Q R V A I A R A
F I R D T P I L F L D E A V S A L D I V H R N

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

NCBI **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:29
P S A P T A F V Y K N M N F D M F C G Q T L G I I G E S G T G K S T L V L L L T K I S V
V E Q K P L L F N G T I R D N L T Y G L Q D E R I D T T L L S G G Q A Q R L C I A R A
L L R K S K I L I L D E C T S A L D S V S S S

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:30
Y K P D S P V I L D N I N I S I K Q G E V I G I V G R S G S G K S T L I K L I Q R V G V V
L Q D N V L L N R S I I D N I S L A P G M S G E Q G A G L S G G Q R Q R I A I A R A L V
N N P K I L I F D E A T S A L D Y A S E H

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:31
IPAPRKHLLKNVCGVAYPGELLAVMGSSGAGKTTLLNALAFR
CAYVQQDDLFIGLIAREHLIFQAMVRPGRVKGLSGGERKRLAF
ASEALTDPPLLICDEPTSGLDSFTAH

Sequence 2=application SEQ ID NO:1
GLEISEEINEEDLKECFF

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:32
K S L G N L K I L D R V S L Y V P K F S L I A L L G P S G S G K S S L L R I L A G M S F
V F Q H Y A L F K H M T V Y E N I S F G L R L R F E Y P A Q L S G G Q K Q R V A L A
R S L A I Q P D L L L D E P F G A L D G E L R R

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

NCBI Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:33
QDVAESTRLGPLSGEVRAGRILHLVGPNGAGKSTLLARIAGYL
SQQQTPPFATPVWHYLTLHQHDKTRGRSTNQLSGGEWQRVRL
AAVVLQITLLLLDEPMNSLDVAQQSA

Sequence 2=application SEQ ID NO:1
GLEISEEINEEDLKECFF

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:34
F Y Y G K F H A L K N I N L D T A K N Q V T A F I G P S G C G K S T L L R T F N K V G
M V F Q K P T P F P M S I Y D N I A F G V R L F H Q S G Y S L S G G Q Q Q R L C I A R
G I A I R P E V L L L D E P C S A L D P I S T G

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 110

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:35
R R Y G G H E V L K G V S L Q A R A G D V I S I I G S S G S G K S T F L R C I N F G I M
V F Q H F N L W S H M T V L E N V M E A P I Q V G K Y P V H L S G G Q Q Q R V S I A
R A L A M E P D V L L F D E P T S A L D P E L V G

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:36
K A W G E V V V S K D I N I D I H E G E F V V F V G P S G C G K S T L L R M I A G V G
M V F Q S Y A L Y P H L S V A E N M S F G L K P A D R K P K A L S G G R Q Q R V A I
G R T L V A E P S V F L L D E P L S N L D A A L R V

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:37
TPDGDVTAVNDLNFTLRAGETLGIVGESGSGKSQTAFALMGIS
MIFQDPMTSLNPYMRVGEQLMEVLMKMYPHEFSGGMRQRVM
IAMALLCRPKLLIADEPTTALDVTVQA

Sequence 2=application SEQ ID NO:1
GLEISEEINEEDLKECFF

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:38
Q P P K T L K A V D G V T L R L Y E G E T L G V V G E S G C G K S T F A R A I I G I Q
M I F Q D P L A S L N P R M T I G E I I A E P L R N R Y P H E F S G G Q C Q R I G I A R A L
I L E P K L I I C D D A V S A L D V S I Q A

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

NCBI **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:39
K A V P G V K A L S G A A L N V Y P G R V M A L V G E N G A G K S T M M K V L T G
A G I I H Q E L N L I P Q L T I A E N I F L G R E F V D K L V G D L S I G D Q Q M V E I A
K V L S F E S K V I I M D E P T C A L I D T E T E

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:40
V D N L C G P G V N D V S F T L R K G E I L G V S G L M G A G R T E L M K V L Y G I S
E D R K R D G L V L G M S V K E N M S L T A L R Y E Q A I G L L S G G N Q Q K V A I
A R G L M T R P K V L I L D E P T P G V D V G A K K

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:41
L T G A R G N N L K D V T L T L P V G L F T C I T G V S G S G K S T L I N D T L F T Y T
G V F T P V R E L F A G V P E S R A R G Y T P G G Q S A T T L S G G E A Q R V K L A R
E L S K R G L Y I L D E P T T G L H F A D I Q Q

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:42
K S Y G G K I V V N D L S F T I A A G E C F G L L G P N G A G K S T I I R M I L G I G I
V S Q E D N L D L E F T V R E N L L V Y G R Y F N T R V A D L S G G M K R R L T L A
G A L I N D P Q L L I L D E P T T G L D P H A R H

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found

Sequence 1=Tsui SEQ ID NO:43
A Y L G G R Q A L Q G V T F H M Q P G E M A F L T G H S G A G K S T L L K L I C G I
G M I F Q D H H L L M D R T V Y D N V A I P L I I A K N F P I Q L S G G E Q Q R V G I A
R A V V N K P A V L L A D E P T G N L D D A L S E

Sequence 2=application SEQ ID NO:1
G L E I S E E I N E E D L K E C F F

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Sequence 1 lcl|seq_1 **Length** 111

Sequence 2 lcl|seq_2 **Length** 18

No significant similarity was found